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**THE GENUS *UNIO* PHILIPSSON 1788, (*MOLLUSCA*, *BIVALVIA*)
IN ITALY. BIOMETRICAL STUDY OF SIX POPULATIONS, ON
THE BASIS OF THEIR CONCHOLOGICAL CHARACTERS. (***)**

KEY WORDS: Mollusca, Bivalvia, genus *Unio*, Italy, Conchological Characters, Biometrical Study

Summary

This research has been performed on 12 conchological variables taken from 328 adult specimens of the genus *Unio* collected in the following places of the Italian peninsula: (1) lake Maggiore; (2) little lakes to the south of lake Como: Alserio, Annone, Pusiano and Segrino; (3) Po di Tolle river, in Venetia; (4) Staggia stream, in Tuscany; (5) Paglia river, between Tuscany and Latium; (6) Bradano river, in Basilicata. Populations 1-5 include *U. elongatulus* PFEIFFER, 1825 and *U. glaucinus* PORRO, 1838. On the contrary, the morphological type of population 6 is clearly different from the two above-mentioned and, as far as we know, never has been reported in malacological literature.

Two distinct biometric methods were used. The first method, called «demogenetic» and proposed since at least three decades by the Italian anthropologist Sacchetti (cf. SACCHETTI, 1943, 1947, 1950, 1955, 1981; BEER & SACCHETTI, 1952; ZANFRÀ, 1960; FONDI, 1980, 1983) is based upon the simple determination of the average probability of transvariation, i.e. the degree of overlapping — or of «typological adherence» — between the variability curves of the corresponding characters. The other method is the well-known multivariate morphometric technique of the principal components.

In spite of the differences that distinguish the theoretical and methodological bases of these statistical techniques, the results were identical. The shells of the central-northern populations (1-5) turned out to be very similar, while clearly differed from the ones of the southern population (6) by the stronger development of the rear-umbonal parts. In full accordance with the biochemical data of BADINO & CELEBRANO (1981), all the central-northern populations can therefore be gathered in a single species, may be referable to *U. elongatulus*. On the contrary, the Bradano population may turn out to belong to another species.

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As the freshwater invertebrates manifest, on the whole, unusually elastic phenotypes, it cannot be excluded that the morphological unities revealed by means of the biometrical analysis are merely cases of phenotypic discontinuity, or polymorphism, within the same taxon. If so, these unities would be clearly devoid of any true systematic significance. However, while certainly admitting this possibility for the unities which are distinguishable within the complex of the central-northern populations, we doubt it may be extended either to the southern population, so remarkably different from all the formers.

Riassunto

Questa ricerca è stata effettuata su 12 variabili rilevate dalla conchiglia di 328 esemplari adulti del genere *Unio* raccolti nelle seguenti località dell'Italia peninsulare: (1) lago Maggiore; (2) laghetti di Alserio, Annone, Pusiano e Segrino, nell'immediato sud del lago di Como; (3) Po di Tolle; (4) torrente Staggia, nei pressi di Siena; (5) fiume Paglia, al confine tra la Toscana e il Lazio; (6) fiume Bradano, in Basilicata. Le popolazioni 1-5 includono *U. elongatulus* PFEIFFER, 1825 e *U. glaucinus* PORRO, 1838. Al contrario, il tipo morfologico della popolazione 6 risulta notevolmente diverso da quello dei due suddetti e, per quanto ne sappiamo, non è mai stato segnalato nella letteratura malacologica.

Sono stati utilizzati due differenti metodi biometrici. Il primo di questi, denominato « demogenetico » e proposto da almeno tre decenni dall'antropologo Sacchetti (cf. SACCHETTI, 1947, 1950, 1955, 1981; BEER & SACCHETTI, 1952; ZANFRÀ, 1960; FONDI, 1980, 1983), si basa sulla semplice determinazione della probabilità media di transvariazione, vale a dire il grado di sovrapposizione — o di « aderenza tipologica » — tra le curve di variabilità dei caratteri corrispondenti. L'altro metodo consiste nella ben nota tecnica di morfometria multivariata delle componenti principali.

Malgrado le differenze che distinguono le basi teoretiche e metodologiche di queste tecniche statistiche, i risultati sono stati i medesimi. Le conchiglie delle popolazioni centro-settentrionali (1-5) si sono rivelate molto simili tra loro, ma ben differenziate da quelle della popolazione meridionale (6) per lo sviluppo notevolmente più accentuato delle parti retro-umbonali. In pieno accordo con i dati biochimici di BADINO & CELEBRANO (1981), tutte le popolazioni centro-settentrionali possono dunque venir raccolte in un'unica specie, probabilmente riferibile ad *U. elongatulus*. Al contrario, la popolazione del Bradano può dimostrare di appartenere ad un'altra specie.

Poichè gli invertebrati d'acqua dolce manifestano, nel loro complesso, fenotipi insolitamente elastici, non si può escludere che le unità morfologiche rilevate dall'analisi biometrica siano semplicemente casi di discontinuità fenotipica, o di polimorfismo, nell'ambito del medesimo taxon. Se così fosse, è chiaro che tali unità sarebbero prive di qualsiasi significato sistematico. In ogni caso, pur ammettendo senz'altro questa possibilità per le unità che si distinguono in seno al complesso delle popolazioni centro-settentrionali, dubitiamo che essa possa venire estesa anche alla popolazione meridionale, così notevolmente differenziata da tutte le altre.

Introduction

Since there is not, in the *Unionidae*, a reproductive apparatus so well distinct from the other soft anatomical structures, as in most of Mollusca, the authors who — from Linné until today — dealt with the systematics of these animals, directed their attention essentially on the shell morphology of few specimens, creating an exorbitant number of « species », the majority of which has been eliminated in the most recent revisions. In this way, from more than 120, the Italian species of the genus *Unio* have been reduced to

5-8 (ALZONA, 1971) and even to only 1 (HAAS, 1940; ZILCH, 1967; CASTAGNOLO, FRANCHINI & GIUSTI, 1981). Furthermore, the study of biosystematics founded on populations and also open to the consideration of non-morphological characters (cf., e.g., the biochemical enquires of BADINO, 1980, and BADINO & CELEBRANO, 1978, 1981, based on the enzymatic polymorphism) offer new prospects and surely promise much more reliable results than those up to now attained.

Recently, shells of four italian populations of *Unio* from the rivers Po, Staggia, Paglia and Bradano were biometrically studied by CASTAGNOLO, FEDERICO & MINERVINI (1977). In that study, the regression straight lines of 4 linear variables were compared pairwise. The results were that, at times, differences between geographically close populations (e.g. Staggia and Paglia) were more remarkable than between geographically far apart populations (e.g. Staggia and Bradano). In any case, the distances between the lines did not appear so great as to suggest a subdivision of the examined samples into two or more definitely distinguishable taxa. The two following and opposite interpretations were therefore drawn: (1°) the biometric characters retained for consideration had no systematic significance and did not lend themselves to meaningful distinctions of the populations under study; (2°) the same characters had a systematic value, however limited to very low levels, subspecific, of the taxonomic scale. And it was concluded with a note of distrust towards the type of biometric technique used, stating that it did not seem to have succeeded in adequately representing those peculiarities of the shell which — when observed together by the specialist — allow him however to recognize distinct morphological types inside the complex of forms taken into consideration.

The present study, directly related to the other just mentioned, aims at demonstrating that biometry is perfectly capable of representing the peculiarities of whatever natural group of organisms. However, if one wants to get a satisfactory picture of the similarities/differences existing between the organic groups, it will not be sufficient to compare characters pairwise each time. More appropriate and comprehensive statistical techniques ought to be used, in order to compare simultaneously an adequate number of characters.

For this reason, we utilized two different biometric techniques of the above-mentioned type, i.e. the one called «demogenetic», proposed since at least three decades by the italian anthropologist Sacchetti (cf. SACCHETTI, 1943, 1947, 1950, 1955, 1981; BEER & SACCHETTI, 1952; ZANFRÀ, 1960; FONDI, 1980, 1983) and based upon the simple determination of the average probability of transvariation (degree of overlapping, or of «typological adherence», between the variability curves of the corresponding characters), and the well-known multivariate morphometric technique of the principal components (cf. MORRISON, 1967; BLACKITH & REYMENT, 1971). This procedure has already been tried in another study concerning the syste-

matics of the Foraminifera (ZAMPI, FONDI & SCALA, 1980), and in both cases the two methods led to identical results, in spite of the differences that distinguish their theoretical and methodological bases.

Our research was exposed at the IV Congress of the Società Malacologica Italiana (Siena, 6-9 October 1978) (FONDI, SCALA & CASTAGNOLO, 1980).

Material

Shells of 328 sexually mature specimens, approximately of the same age (4-6 years), were measured. The age was determined counting the principal growth-lines on the external side of the shell. Little attention was paid, instead, to possible sexual differences affecting the morphology of the shell, as nobody seems to have succeeded so far in recognizing them in the *Unionidae* (NARDI & BARBIERI, 1977).

The specimens came from the following Italian localities: (1) lake Maggiore, near Arona (n° 30); (2) little lakes south of lake Como: Alserio, Annone, Fusiano and Segrino (since the specimens gathered from these lakes, geographically very close to each other, were practically undistinguishable in a preliminary and accurate examination, we considered them as a single population) (n° 36); (3) river Po (Po di Tolle) near its mouth, a few km before the built-up area of Scardovari (Rovigo) (n° 70); (4) Staggia stream, near Poggibonsi (Siena) (n° 70); (5) Paglia river, near Acquapendente (Viterbo) (n° 52); (6) Bradano river, near its mouth into S. Giuliano lake (Matera) (n° 70).

Biometric characters

The following 10 linear variables were taken into consideration: (A) distance umbo — anterior margin of the shell; (B) height at the umbo; (C) height at the posterior end of the ligament; (D) distance umbo - posterior margin of the shell; (E) width; (F) distance between the adductor muscles; (G) distance umbo — anterior end of the hinge; (H) distance umbo — posterior end of the hinge; (I) distance umbo — anterior end of the ligament; (J) distance umbo — posterior end of the ligament. Two goniometric variables, α and β , were added to these. They measure the amplitude value of the shell's margin corresponding to the inhalant and exhalant openings and to the same margin plus the rear ligamentary area respectively (Fig. 1).

The goniometric variables, however, being difficult to measure, are subjected to high probability of recording errors and — whether taken or not into account — results reached are not so different as to make believe they are very relevant in determining the systematic structure of the *Unio* complex. To make the reading of the

diagrams of typological adherence easier, we excluded these variables from the latter and utilized them only in the principal components method.

As the genetics of *Bivalvia* is still today most unexplored, it cannot be assured that the characters we chose have a real systematic or « demogenetic » value, i.e. that, in addition to being constant in the populations, they also have an effective genotypical foundation. However, until the contrary is proved, nothing can prevent on considering them as such for the systematics of *Bivalvia* in general. In fact these characters, the goniometric excepted, seem to be apt to be recorded from all the representatives of this class of Mollusca.

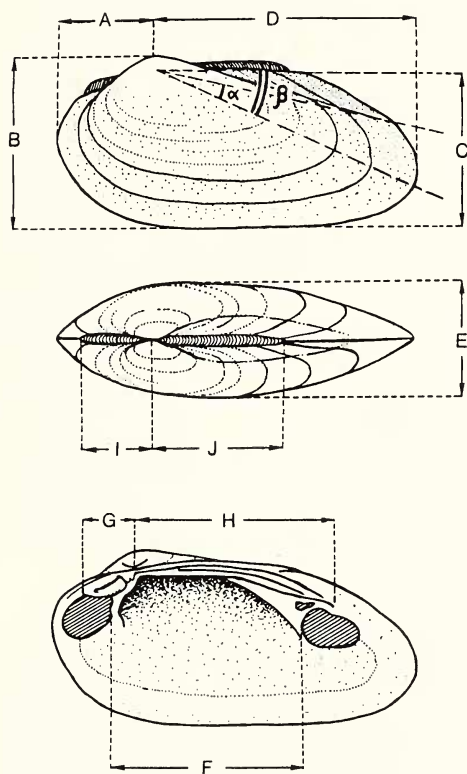


Fig. 1 - Biometric characters taken from the shell.

Statistical analysis

a) Elementary description of the six populations.

Two of the essential statistical indexes, mean and standard deviation, are shown in table 1. They deal with the marginal distributions of the six 12-variate systems here compared, which looked reasonably normal when the values of skewness and kurtosis were exa-

GROUPS			1	2	3	4	5	6
individuals			30	36	70	70	52	70
C H A R A C T E R S	A	M	10.539	14.839	20.754	18.297	23.187	11.571
		σ	0.952	2.712	2.865	3.782	2.976	1.988
	B	M	25.400	34.000	36.786	30.814	36.461	21.014
		σ	1.720	3.617	4.155	3.797	3.283	2.529
	C	M	26.133	34.389	33.100	30.929	33.892	20.686
		σ	1.835	3.080	3.627	3.908	2.613	2.904
	D	M	47.467	58.833	61.229	46.800	55.353	29.271
		σ	4.564	6.807	7.825	6.517	4.872	3.807
	E	M	19.400	24.639	24.529	19.471	23.794	12.686
		σ	1.491	2.945	3.355	2.808	2.190	1.676
	F	M	33.033	42.639	45.171	33.086	41.324	21.300
		σ	2.742	5.170	5.395	4.621	4.255	2.801
	G	M	6.667	8.694	10.143	7.514	8.324	6.371
		σ	0.897	1.350	1.363	1.259	1.200	1.133
	H	M	30.200	59.000	40.386	31.629	37.716	18.600
		σ	2.771	4.604	4.877	4.741	3.690	2.625
	I	M	9.700	13.132	14.657	11.557	12.578	8.029
		σ	0.832	2.043	2.102	2.035	1.467	1.284
	J	M	28.733	37.528	39.743	29.229	35.598	17.857
		σ	2.813	4.628	5.200	4.436	4.098	2.627
	α	M	11.367	9.306	8.957	12.614	12.346	9.957
		σ	1.832	1.997	1.101	1.552	1.479	1.535
	β	M	25.600	22.083	20.557	28.843	28.404	27.000
		σ	4.507	3.295	1.696	2.539	2.356	2.823

Table 1 - Mean (M) and standard deviation (σ) of each character for each population (in mm).

mined. Although this fact does not guarantee completely the multi-normality of the system, it is well known that the principal components method is rather « robust », in so far as it does not react in an important way to non-macroscopic deviations of the data-system from the multi-normal model, for what concerns the descriptive power of tolerance ellipses.

b) *Average probability of typological adherence.*

The systematic distance among the *Unio* populations can be determined simply by means of the Sacchetti's index. This index, T_n or TA, measures the probability of transvariation, or of « typological adherence », between the variability curves of corresponding characters and varies between 1 (complete adherence — indistinct characters — identical taxa) and 0 (no adherence — distinct characters — separate taxa) (*). As TA is valid only for gaussian curves, the empirical variability curves must be normalized when skewness and kurtosis are considerable.

The index of typological adherence can be mathematically expressed, for each character, in the following way:

$$TA = 1 - 2 \Theta \frac{CIRV}{2}$$

where Θ is the well known integral function of normal variability formulated by Gauss,

$$\Theta(t) = \frac{1}{\sqrt{2\pi}} \int_0^t e^{-\frac{t^2}{2}} dt,$$

and CIRV is the so-called « coefficient of intergroup relative variability » proposed by Sacchetti in 1942. This coefficient consists in the following ratio:

$$CIRV = \frac{\Delta_{(Me)}}{\sigma_{(Me)}}$$

where the numerator express the *average intergroup variability* (mean difference between the means of the single groups or populations and the one of the « median group ») and the denominator the *average intragroup variability* (median value of the standard deviations showed by the single groups or populations) (**).

In definitive, as can be seen easily, the procedure to calculate

(*) In reality, owing to the well-known asymptotical nature of the gaussian curves, TA only can « tend » to 0 without ever reaching it in an absolute way.

(**) The choosing of the *median* value (Me) instead of the simple average value (M) is immediately intelligible, when the properties of the statistical concept of median are remembered. In a set of values, as in set of groups, the median occupies the *central* position, so that the mean difference between it and the others always is the slightest. When the set of values has a normal distribution, mean and median coincide; but in a set (or complex) of groups more or less strongly differentiated one from another, a normal distribution is not the rule.

CIRV does not need more than the knowledge of the mean and the standard deviation of each character for each population (Table 1). On the other hand, the passage from the CIRV values to the corresponding TA values becomes practically immediate by means of a suitable numerical table published by Sacchetti (1950).

The reference to the « median group » as representative of the entire complex of the n groups or populations under study, although allowing a maximum simplification — reducing the number of comparisons from $n(n-1)$ to n (in our case, 6 instead of 30!) — is not

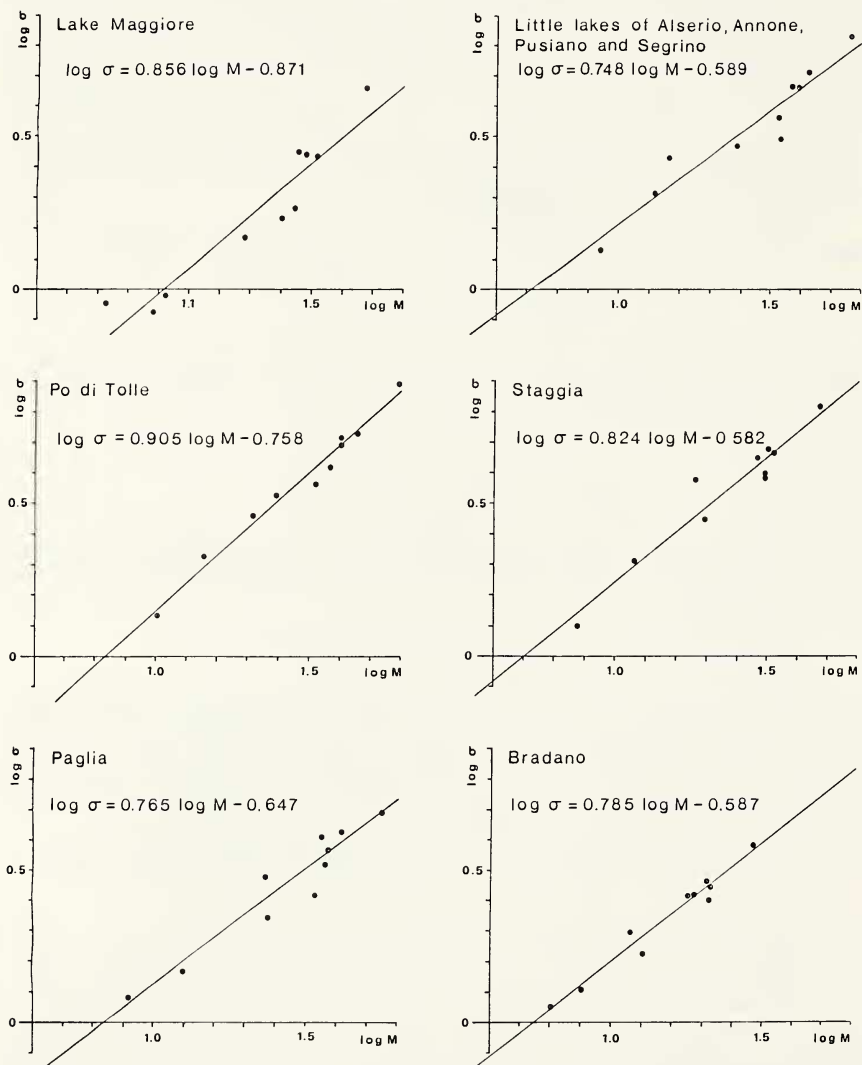


Fig. 2 - Linear logarithmic relations between the means and the standard deviations of the various characters in each *Unio* population.

necessarily a sheer abstraction. As a matter of fact, such a reference permits to consider each group, rather than disconnected and independent of the others, as though it and the others are integrative elements (i.e. a number of taxa) of the same system or systematic complex (i.e. a more elevated taxon). Indeed this is the case in nature, if we follow the opinion of many biologists who, since ever before Darwin, admit the reality of a biological Natural System (cf. SNEATH & SOKAL, 1973, p. 19-27; von BERTALANFFY, 1971; JANTSCH, 1980).

The mean (median) intragroup variabilities for the entire *Unio* complex (denominators of the CIRVs) were not calculated from the empirical, but from the *theoretical* standard deviations of the characters determined for each population. In fact, it has been widely demonstrated (SACCHETTI, 1940, 1941, 1949; SACCHETTI & FONDI, 1981) that exists a tendentially linear relation between the logarithms of the means and of the standard deviations of the characters exhibited by the different biological organization. This relation is expressed by the equation

$$\log \sigma = b \log M \pm \log K$$

where the intercept $\log K$ is different from group to group, while the slope b generally maintains itself around the empirical value of 0.8.

The linear logarithmic relations between the means and the standard deviations of the various characters within each *Unio* population are shown in fig. 2. In their turn, the equations expressing these relations easily permit to obtain the *theoretical* standard deviations corresponding to the empirically recorded distributions. So we can get away from the raw individual phenomenon and make reference to the natural *norm*, or law, of which that phenomenon merely represents a more or less adherent expression (see the different deviations of the points from the interpolatory straight lines).

UNIO SPURIOUS SYSTEM	C	H	A	R	A	C	T	E	R	S
	A	B	C	D	E	F	G	H	I	J
Me	16.568	32.407	32.015	51.410	21.633	37.205	7.919	34.673	12.068	32.414
$\sigma_{(Me)}$	2.336	3.786	3.707	5.475	2.785	4.282	1.260	4.066	1.774	3.846
$\Delta_{(Me)}$	4.215	5.003	3.606	8.646	3.568	6.953	1.102	9.446	1.847	6.175
CIRV (Me)	1.804	1.321	0.973	1.579	1.281	1.624	0.875	2.323	1.041	1.606
TA (Me)	0.367	0.509	0.627	0.430	0.522	0.417	0.662	0.245	0.603	0.422

Table 2 - Spurious complex. Average intergroup typological adherence between the characters of the various populations and the corresponding ones of their « median population ».

In this way, after having the CIRVs « normalized » by means of the theoretical standard deviations, we can pass from them to the relative TAs between the characters of the single populations and the corresponding ones of the « median population » (Table 2).

The average typological adherence, or $M_{(TA)}$, resulting from the 10 characters taken into consideration, is 0.476. This value, however, still concerns a systematically spurious complex, i.e. a complex of which the internal systematic structure is still unknown. To define this structure, we need a complete picture showing exactly the relative positions of the single populations, with reference to the entire complex (or, as we postulated, to the « median population ») which integrates them. This can be obtained directly from the table 2, merely substituting the numerators of the CIRVs by the simple 6 differences $M_i - M_e$ (mean of each group minus the mean of the « median group ») and calculating the relative values of ${}_{(X)}TA_{(Me)}$. These values are plotted versus the single characters in the diagram of fig. 3.

Before examining this diagram, we must explain why the characters are not arranged in it alphabetically. In fact, the arrangement of the characters follows the decreasing order of their average *intragroup typological adherence* (ITA), or average degree of transvariation between the individuals composing a biological group and the « mean individual » of the group itself. This new index has

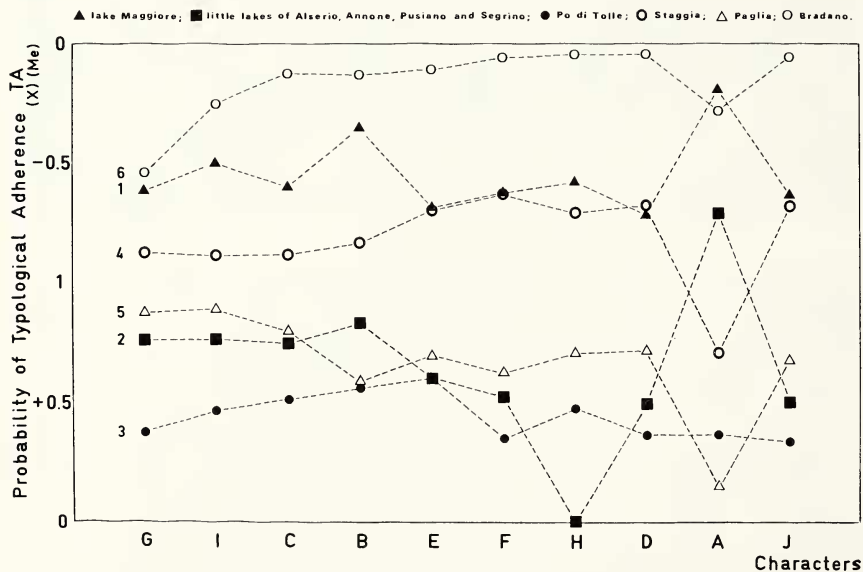


Fig. 3 - Probability of typological adherence between the characters of each population and the corresponding ones of the « median group », ${}_{(X)}TA_{(Me)}$. The arrangement of the characters follows the decreasing order of their average intragroup typological adherence, or ITA (cf. fig. 4). The diagram illustrates the relative positions of the *Unio* populations with reference to the wider natural complex which integrates them all.

been recently conceived and personally communicated to one of us (R.F.) by Sacchetti (cf. SACCHETTI, 1984). It constitutes a true index of absolute variability and is calculated, for each group or population, from a particular CIRV having at the numerator the following expression (cf. GINI, 1939):

$$\Delta_{(M)} = \frac{2}{\sqrt{\pi}} \sigma : \sqrt{2} = \frac{1}{\sqrt{\frac{\pi}{2}}} \sigma = 0.7979 \sigma$$

and at the denominator one of the following standard deviations:

σ_t OR σ_r .

σ_t is the « theoretical » standard deviation (obtained from the equation $\log \sigma = b \log M \pm \log K$) and σ_r is the so-called « reference » standard deviation (obtained from the same equation but assuming $\log K = 0$). In this way, we have two CIRVs, CIRV_t and CIRV_r, and consequently two ITA, ITA_t and ITA_r, at our disposal. The formers will be useful in comparisons within groups or complexes, and the latter in comparisons among groups.

In the diagram of fig. 4 are plotted, for each *Unio* population, the values of ITA_r of each character and their average values from the whole set of characters (Table 3). All the populations have practically the same ITA_r, with the only exception of the population from lake Maggiore which is clearly more variable.

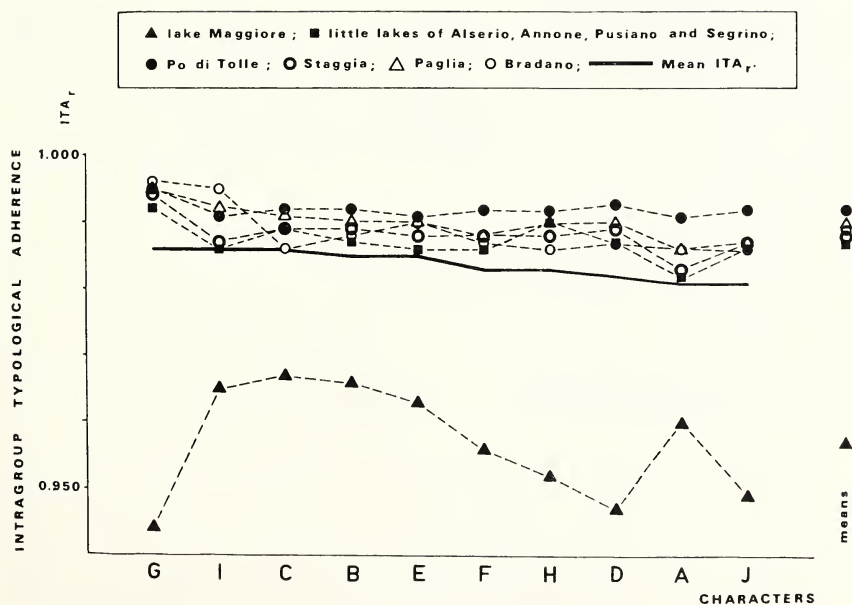


Fig. 4 - Probability of intragroup typological adherence, i.e. between the characters of the individuals composing each *Unio* population and the corresponding characters of the « mean individual » of the population itself.

GROUP		1	2	3	4	5	6	$M_{(ITA)}$
S R E T C A R A H C	A	0.960	0.982	0.991	0.983	0.986	0.986	0.981
	B	0.966	0.987	0.992	0.989	0.990	0.988	0.985
	C	0.967	0.989	0.992	0.989	0.991	0.986	0.986
	D	0.947	0.987	0.993	0.989	0.990	0.987	0.982
	E	0.963	0.986	0.991	0.988	0.990	0.990	0.985
	F	0.956	0.986	0.992	0.988	0.988	0.987	0.983
	G	0.944	0.992	0.995	0.994	0.995	0.996	0.986
	H	0.952	0.990	0.992	0.988	0.990	0.986	0.983
	I	0.965	0.986	0.991	0.987	0.992	0.995	0.986
	J	0.949	0.986	0.992	0.987	0.987	0.986	0.981
$M_{(ITA)}$		0.957	0.987	0.992	0.988	0.990	0.989	0.984

Table 3 - Average intragroup typological adherence (ITA_r), for each population, between the characters of the various individuals and the corresponding ones of the « average individual ».

Now we can turn back to the diagram of fig. 3. It shows that the values of TA between the characters of the single 6 populations and the corresponding ones of the « median population » are perfectly adequate to give a reliable picture of the relative positions of the *Unio* populations within their complex. Three morphological units are more or less well distinguishable in the complex, namely: (a) Bradano; (b) lake Maggiore and Staggia; (c) Paglia, little lakes near Como and Po di Tolle.

As these units can be hierarchically arranged according to the decreasing values of the average typological adherence to their « median groups », or $M_{(TA)}$, a taxogram has been constructed (Fig. 5). It shows the Bradano population clearly apart from all the others, which, in their turn, form two morphologically very close units (Ia and Ib, in the figure). The values of $M_{(TA)}$ and $\sigma_{(TA)}$ concerning the units Ia, Ib, II and III, are reported in table 4.

c) Multivariate analysis through the principal components.

Using the principal components technique (cf. DAGNELIE, 1975; MORRISON, 1976), the six groups were simultaneously subjected to the same linear transformation of co-ordinates and each one represented in the same diagram with its own individuality (Fig. 6). In this way, the 6 *Unio* populations were forced to pass from Euclidean $R^{(12)}$ to $R^{(2)}$ without any relevant loss of data. In the $R^{(2)}$, measured in a first and a second principal component, PC_1 and PC_2 (i.e. linear combination of the 12 variables-values — x_1, \dots, x_{12} — with coeffi-

cients given by the eigen-vectors of the matrix S), the two new variables are independent by construction. Observations expressed in terms of principal components concerning the *single* populations were not, however, necessarily independent, so that it is possible and allowed the plotting of tolerance ellipses corresponding to these latters.

As a large number of characters (10 linear and 2 goniometric) was taken into consideration, it is impossible to publish all the essential data of the analyses carried out with the principal components method. Those interested in getting the detailed numerical documentation could ask for it directly to one of us (R.F.). However, the equations of the two principal components which substantially reproduce the variability of the mixed sample obtained combining the six original samples together, are the following:

$$PC_1 = 0.312 A + 0.314 B + 0.305 C + 0.318 D + 0.318 E + 0.322 F + 275 G + 0.320 H + 0.306 I + 0.320 J - 0.048 \alpha - 0.152 \beta;$$

$$PC_2 = 0.082 A + 0.108 B + 0.193 C + 0.023 D + 0.057 E + 0.014 F - 0.155 G + 0.064 H - 0.007 I + 0.017 J + 0.720 \alpha + 0.628 \beta.$$

The tolerance ellipses — which, in our case, « seize » 90% of the information concerning every population — overlap in a highly

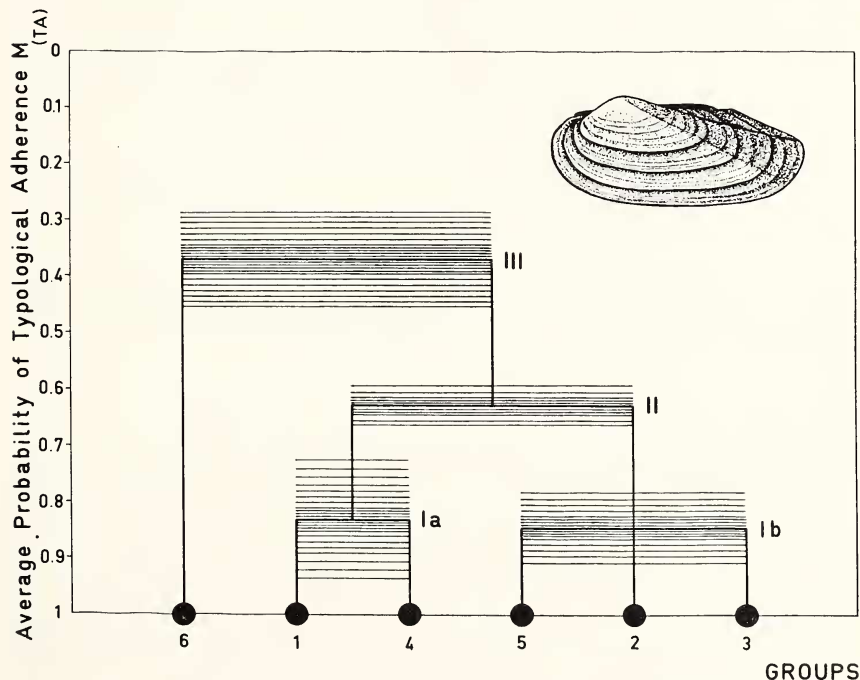


Fig. 5 - Taxogram of the *Unio* complex. The various systematic unities (Ia, Ib, II and III) are hierarchically arranged according to the decreasing values of the average probability of typological adherence, $M_{(TA)}$, between their characters and the corresponding ones of their « median groups » of reference. $\sigma_{(TA)}$ are indicated by the series of lines. The diagram shows the Bradano population (n. 6) clearly apart from all the others, which, in their turn, form two very close morphological unities (Ia and Ib, in the figure).

comp lexes		Ia	Ib	II	III
S R E T A C T A R A H C H C	A	0.318	0.520	0.557	0.494
	B	0.680	0.886	0.602	0.400
	C	0.836	0.952	0.768	0.392
	D	0.973	0.864	0.607	0.200
	E	0.994	0.953	0.647	0.314
	F	0.997	0.881	0.553	0.235
	G	0.837	0.786	0.679	0.710
	H	0.919	0.927	0.629	0.226
	I	0.749	0.828	0.668	0.500
	J	0.970	0.867	0.567	0.217
	M _{TA}	0.831	0.846	0.628	0.369
	σ_{TA}	0.199	0.120	0.063	0.156

Table 4 - Reconstructed complex. Average intergroup typological adherence, $M_{(TA)}$, between the characters of the various systematic unities (Ia, Ib, II and III, in fig. 5) and the corresponding ones of their « median unities ».

noticeable way (Fig. 6). Only the Bradano population can be clearly distinguished from all the others. Moreover, if we neglect the PC_2 (this principal component has a saturation power of only 13.97%), it can be observed, when we project the centres of the ellipses exclusively along the PC_1 axis (which saturation power is 78.28%), that the relative positions of the *Unio* populations allow the distinction of the following groups: (a) Bradano; (b) lake Maggiore and Staggia; (c) Paglia, little lakes near Como and Po di Tolle. In particular, the Bradano population is notably away from (b) and (c), which, on the other hand, are not very different from each other.

This relative disposition of the 6 populations fits exactly with the one obtained on the basis of the average typological adherence (see the taxogram of fig. 5), namely without considering the correlation among the characters.

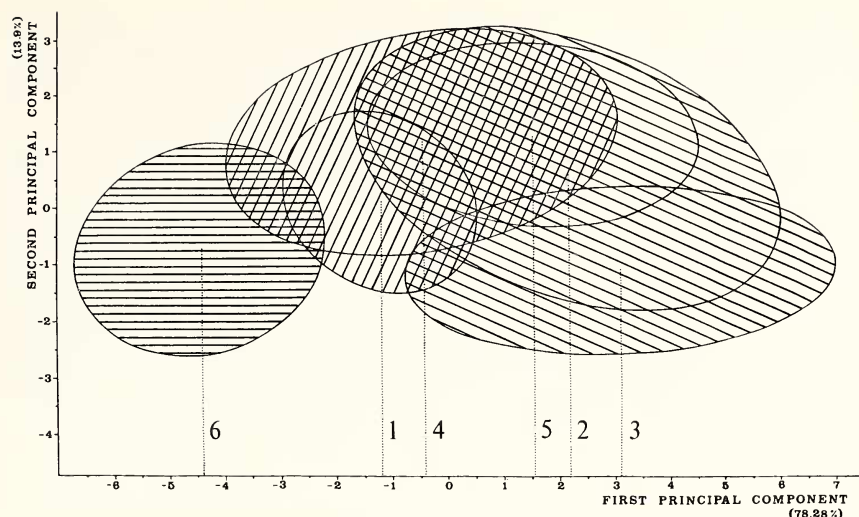


Fig. 6 - First principal component (PC_1) versus second principal component (PC_2) on the correlation matrix of the 12 variables (complex of the *Unio* populations). Tolerance ellipses at 90% on the principal component scores — calculated on the complex — of the six populations. Values in parenthesis indicate the saturation (or explanation) percentage of each principal component. The relative disposition of the populations fits very well with the one obtained in fig. 5.

Systematic implications

Within the limits of the informations provided by the conchological material we considered (which is however, until now, the richest ever examined with a quantitative-systematic aim in our country), we feel that in peninsular Italy not more than two types of *Unio* can be recognized: the one related to the whole of the groups 1-5 (lake Maggiore, little lakes near Como, Po di Tolle, Staggia and Paglia), very similar and difficult to distinguish one from the others, and the one corresponding to the group 6 (Bradano), chiefly characterized by the scanty development of the rear-umbonal parts (variables D, J, H and F), as well by the smaller general size (Fig. 7).

The first of these two types can easily be identified with *Unio elongatulus* PFEIFFER 1825, i.e. the oldest among the numerous Italian species proposed until today (***). But also *U. glaucinus* PORRO 1838 and the three species dubiae quoted by ALZONA (1971) - *U. eucallistellus* BOURGUIGNAT 1883, *U. padanus* BOURGUIGNAT 1883 and

(***) There are still not, however, research works demonstrating a real correspondence between the Dalmatian type-populations of *U. elongatulus* and the Italian ones or, on the other hand, confirming the validity of this species with respect to older European species like *U. crassus* (RETZIUS, 1788).

U. bourguignatianus ADAMI 1885 - clearly correspond to the same form. So, also on the basis of the concordant results brought forward by the biochemical enquiry of BADINO & CELEBRANO (1981), we feel that they should be eliminated and included in *U. elongatulus*.

As regards the Bradano population, we think that it may constitute another species, as far as we know never reported before in the malacological literature. No type of the rich Monterosato and Rigacci collections at the Museo di Zoologia del Giardino Zoologico in Rome resembles the form of Bradano in a reliable way. In fact, it seems that — until today — no zoologist has taken into consideration *Unio* populations living along the eastern side of the Apennines to the south of the Panaro river, in Emilia. And the observations seem to be missing even as regards the western side of the Apennines to the south of Salerno.

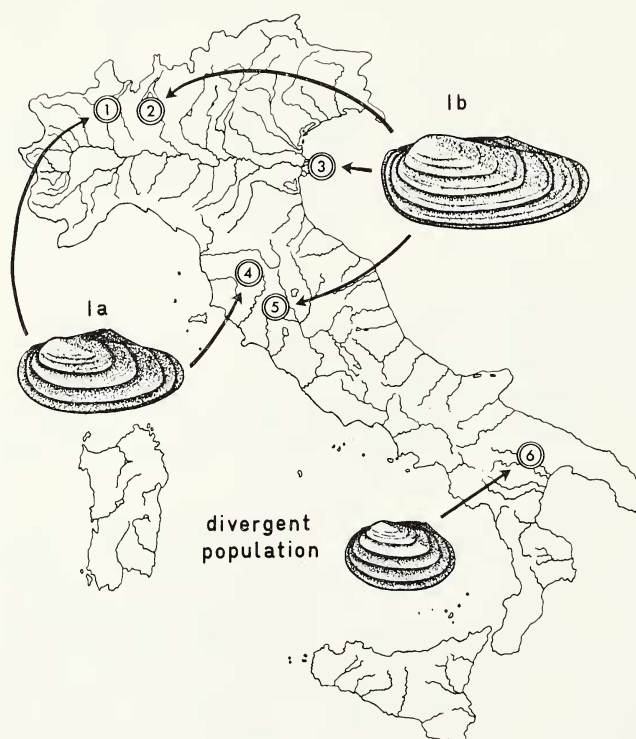


Fig. 7 - Place of origin of the analysed *Unio* populations: (1) lake Maggiore; (2) little lakes of Alserio, Annone, Pusiano and Segrino, to the south of lake Como; (3) Po di Tolle; (4) Staggia; (5) Paglia; (6) Bradano. The drawings of the three shells represent the types of the three morphological unities resulting from the diagrams of fig. 5-6. These types have been constructed on the basis of the average values of the characters taken into consideration.

While waiting for further biochemical enquiries confirming or disproving this hypothesis, we must take another possibility into serious consideration. As the freshwater invertebrates manifest, on the whole, unusually elastic phenotypes (cf., e.g., BROOKS 1957), it cannot be excluded that the morphological unities revealed by means of the biometrical analysis are merely cases of phenotypic discontinuity, or polymorphism, within the same taxon. If so, these unities would be clearly devoid of any true systematic significance.

This possibility seems particularly strong for the unities Ia and Ib within the complex of the central-northern *Unio* populations (Fig. 5, 6, 7), as they both include spatially far apart demes and nevertheless strangely maintain themselves geographically contiguous. We are in doubt, however, that the southern population, so remarkably distinguished from all the formers, may be either interpreted in the same way.

Siena - 15 novembre 1983

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